Please delete the paragraph beginning on line 12 of page 6 and ending on line 6 of page 7 and replace it with the following new paragraph.

One million plaques of a mouse genomic library (bacteriophage library from strain SVJ129, Stratagene, La Jolla, CS) and one hundred thousand plaques of a *D. melanogaster* genomic library were screened with corresponding cDNA probes. Clones were purified and DNA was isolated. Sequencing was carried out using Perkin Elmer thermal cyclers and ABI 377 automated DNA sequencers. DNA pools from a human BAC library (Research Genetics, Huntsville, AL) were screened by PCR with *NITI* primers (TCTGAAACTGCAGTCTGACCTCA (SEQ ID NO:2) and CAGGCACAGCTCCCCTCACTT (SEQ ID NO:3)) according to the supplier's protocol. The DNA from the positive clone, 31K11, has been isolated using standard procedures and sequenced. Chromosomal localization of the human *NITI* gene was determined using a radiation hybrid mapping panel (Research Genetics) according to the supplier's protocol and with the same primers as above. To map murine *Nitl* gene, Southern blot analysis of genomic DNA from progeny of a (*AEJ/Gn-a* bp^H*/a* bp^H *x M. spretus)*F1 x *AEJ/Gn-a* bp^h*/a* bp^h backcross was performed using a full length murine *Nitl* cDNA probe. This probe detected a unique 2.0 kb DraI fragment in AEJ DNA and a unique 0.75 kb fragment in *M. spretus* DNA. Segregation of these fragments were followed in 180 N2 offspring of the backcross. Additional Mit markers (*D1Mit34, DIMit35*, and *DIMit209*) were typed from DNA of 92 mice by using PCR consisting of an initial denaturation of 4 minutes at 94°C followed by 40 cycles of 94°C for 30 seconds, 55°C for 30 seconds and 72°C for 30 seconds. Linkage analysis was performed using the computer program SPRETUS MADNESS: PART DEUX. Human and mouse*NITI* expressed sequence tag (EST) clones were purchased from Research